GenCore version 4.5

: protein - protein search, using sw model

n on: June 12, 2001, 08:16:48 ; Search time 30.76 Seconds
(without alignments)
390.887 Million cell updates/sec

tle: US-09-452-244-10
rfect score: 1893
quence: 1 MATTQSCQSRSSACSKAAAC.....GFSESITDNFWALEEIWKMQ 351

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 93435 seqs, 34255486 residues

tal number of hits satisfying chosen parameters: 93435

ni DB seq length: 0
xim DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

tabase : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description
1	386.5	20.4	421	1	MYB2_PHYPA	P80073 physcomitre
2	377.5	19.9	399	1	MYBP_MAIZE	P27898 zea mays (m
3	374.5	19.8	228	1	GL1_ARATH	P27900 arabidopsis
4	374	19.8	255	1	MYB3_MAIZE	P20025 zea mays (m
5	370.5	19.6	267	1	MYB1_HORVU	P20026 hordeum vul
6	358	18.9	302	1	MYB3_HORVU	P20027 hordeum vul
7	358	18.9	340	1	MYB1_MAIZE	P20024 zea mays (m
8	348.5	18.4	273	1	MYBC_MAIZE	P10290 zea mays (m
9	340	18.0	252	1	MYBD_MAIZE	P23592 zea mays (m
	290.5	15.3	728	1	MYBA_XENLA	Q05935 xenopus lae
	274.5	14.5	382	1	MYB_AVIMB	P01104 avian myelo
12	274.5	14.5	624	1	MYB_XENLA	Q08759 xenopus lae
13	274.5	14.5	751	1	MYBA_MOUSE	P51960 mus musculu
14	270.5	14.3	752	1	MYBA_HUMAN	P10243 homo sapien
15	266	14.1	640	1	MYB_HUMAN	P10242 homo sapien
16	265.5	14.0	636	1	MYB_MOUSE	P06876 mus musculu
17	265.5	14.0	640	1	MYB_BOVIN	P46200 bos taurus
18	265.5	14.0	641	1	MYB_CHICK	P01103 gallus gall
19	265.5	14.0	757	1	MYBA_CHICK	P52550 gallus gall
20	259.5	13.7	657	1	MYB_DROME	P04197 drosophila
21	250.5	13.2	686	1	MYBB_CHICK	Q03237 gallus gall
22	250.5	13.2	743	1	MYBB_XENLA	P52551 xenopus lae
23	249	13.2	704	1	MYBB_MOUSE	P48972 mus musculu
24	247	13.0	700	1	MYBB_HUMAN	P10244 homo sapien
25	242	12.8	451	1	MYBH_DICDI	P34127 dictyosteli
26	142.5	7.5	757	1	CC5_SCHPO	P39964 schizosacch
27	128	6.8	449	1	MYB1_PHYPA	P80074 physcomitre
28	127.5	6.7	810	1	REB1_YEAST	P21538 saccharomyc
29	127.5	6.7	811	1	BAS1_YEAST	P22035 saccharomyc
30	114.5	6.0	590	1	YM63_YEAST	Q03654 saccharomyc
31	113.5	6.0	595	1	REB1_KLULA	Q05950 kluyveromyc
32	107.5	5.7	2517	1	NCR2_HUMAN	Q9y618 h nuclear r
33	102.5	5.4	562	1	TBF1_YEAST	Q02457 saccharomyc
34	98.5	5.2	2472	1	NCR2_MOUSE	Q9wu42 mus musculu
35	98	5.2	378	1	HAIR_DROVI	P29303 drosophila
36	98	5.2	606	1	HM1D_DROAN	P22544 drosophila
37	97.5	5.2	491	1	IRF3_CHICK	Q90643 gallus gall
38	97	5.1	1169	1	SUV3_DROME	P20193 drosophila
39	95.5	5.0	677	1	UBF1_XENLA	P25979 xenopus lae
40	95	5.0	1597	1	SOL_DROME	P27398 drosophila
41	94	5.0	1723	1	AIM1_HUMAN	Q9y4k1 homo sapien
42	93	4.9	753	1	TKR_DROME	P14083 drosophila
43	93	4.9	1039	1	AG43_ECOLI	P39180 escherichia
44	92.5	4.9	515	1	Y141_HUMAN	Q14154 homo sapien
45	92	4.9	665	1	LAMA_MOUSE	P48678 mus musculu

ALIGNMENTS

RESULT 1
MYB2_PHYPA
ID MYB2_PHYPA STANDARD; PRT; 421 AA.
AC P80073;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MYB-RELATED PROTEIN PP2.
GN PP2.
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94004988; PubMed=8401607;
RA Leech M.J., Kammerer W., Cove D.J., Martin C., Wang T.L.;
RT "Expression of myb-related genes in the moss, Physcomitrella patens.";
RL Plant J. 3:51-61(1993).
CC -!- FUNCTION: POSSIBLE TRANSCRIPTION ACTIVATOR.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- DEVELOPMENTAL STAGE: HIGH RATES OF GROWTH.
CC -!- SIMILARITY: BELONGS TO THE MYB FAMILY.
CC ---

CC ---
DR EMBL; X67050; CAA47435.1; -.
DR PIR; S24244; S24244.
DR HSSP; P01103; 1POM.
DR InterPro; IPR001005; -.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR PROSITE; PS00037; MYB_1; 1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
KW Nuclear protein; DNA-binding; Repeat; Transcription regulation.
FT DNA_BIND 9 61 MYB.
FT DNA_BIND 62 102 MYB.
SQ SEQUENCE 421 AA; 46695 MW; 27A3578578D0F3F4 CRC64;

Query Match 20.4%; Score 386.5; DB 1; Length 421;
Best Local Similarity 51.4%; Pred. No. 7.7e-24;
Matches 76; Conservative 16; Mismatches 43; Indels 13; Gaps 1;

```
Qy      52 KPELRRGPWTVDEDLTLVNYIADNGEGRWNNLARAAGLKRTGKSCRLRWLNYLRPDVKRG 111
           |  ||||||| :||  ||::| :||   |  : : ||| | |||||||| ||||||:|||
Db       9 KVGLRRGPWTSEEDQKLVSHITNNGLSCWRAIPKLAGLLRCGKSCRLRWTNYLRPDLKRG 68

Qy     112 NFSADEQLLILDLHTRWGNRWSKIAQHLPGRTDNEIKNYWRTRVQKHAKQLNCDANSKRF 171
             ||  |: ||||||   |||||:||  |||||||||||||| ||::|  :    | |:
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Applicant's

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Db     69 IFSEAEENLILDLHATLGNRWSRIAAQLPGRTDNEIKNYWNTRLKKRLRSQGLDPNT--- 125

Qy    172 KDAMRYLWMPHLADDVDTIAAANDDDED 199
                  ||  :   :   || :|
Db    126 ----------HLPLEDSKLDDTEDDTDD 143


RESULT   2
MYBP_MAIZE
ID   MYBP_MAIZE     STANDARD;      PRT;   399 AA.
AC   P27898; P27899;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   MYB-RELATED PROTEIN P.
GN   P.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
OC   Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91271238; PubMed=2052542;
RA   Grotewold E., Athma P., Peterson T.;
RT   "Alternatively spliced products of the maize P gene encode proteins
RT   with homology to the DNA-binding domain of myb-like transcription
RT   factors.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4587-4591(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92275319; PubMed=1317315;
RA   Athma P., Grotewold E., Peterson T.;
RT   "Insertional mutagenesis of the maize P gene by intragenic
RT   transposition of Ac.";
RL   Genetics 131:199-209(1992).
CC   -!- FUNCTION: TRANSCRIPTION FACTOR POSTULATED TO REGULATE THE
CC       BIOSYNTHETIC PATHWAY OF A FLAVONOID-DERIVED PIGMENT IN CERTAIN
CC       FLORAL TISSUES.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO THE MYB FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; M73028; AAA33500.1; -.
DR   EMBL; M73029; AAA33501.1; -.
DR   EMBL; Z11879; CAA77939.1; -.
DR   PIR; A39697; A39697.
DR   PIR; B39697; B39697.
DR   PIR; S26150; S26150.
DR   HSSP; P01103; 1POM.
DR   TRANSFAC; T01590; -.
DR   TRANSFAC; T01591; -.
DR   MaizeDB; 69180; -.
DR   MaizeDB; 69181; -.
DR   InterPro; IPR001005; -.
DR   Pfam; PF00249; myb_DNA-binding; 2.
DR   PROSITE; PS00037; MYB_1; 1.
DR   PROSITE; PS00334; MYB_2; 1.
DR   PROSITE; PS50090; MYB_3; 2.
KW   Nuclear protein; DNA-binding; Repeat; Transcription regulation;
KW   Alternative splicing.
FT   DNA_BIND      9     61       MYB.
FT   DNA_BIND     62    102       MYB.
FT   DOMAIN      178    181       POLY-ALA.
FT   DOMAIN      305    311       POLY-LEU.
FT   VARSPLIC     89    152       WSLIASHLPGRTDNEIKNYWNSHLSRQIHTYRRKYTAGPDD
FT                                TAIAIDMSKLQSADRRRGGRTPG -> RHLMIEADYSPPST
FT                                VRCLPRGALAYLTLPRQSPFQTARITYDRIGSALLRSVRFC
FT                                FRCVPSRW (IN SHORT ISOFORM).
FT   VARSPLIC    153    399       MISSING (IN SHORT ISOFORM).
SQ   SEQUENCE   399 AA;  43756 MW;  EE025B00A44CF5D0 CRC64;


  Query Match           19.9%;  Score 377.5;  DB 1;  Length 399;
  Best Local Similarity   34.8%;  Pred. No. 3.8e-23;
  Matches   95;  Conservative   29;  Mismatches   92;  Indels   57;  Gaps    7;

Qy     52 KPELRRGPWTVDEDLTLVNYIADNGEGRWNNLARAAGLKRTGKSCRLRWLNYLRPDVKRG 111
          |  |:|| || :||  | ||||::||| | :| : ||| | |||||||||:|||| |||||
Db      9 KVGLKRGRWTAEEDQLLANYIAEHGEGSWRSLPKNAGLLRCGKSCRLRWINYLRADVKRG 68

Qy    112 NFSADEQLLILDLHTRWGNRWSKIAQHLPGRTDNEIKNYWRTRVQKHAKQLNCDANSKRF 171
          | | :|: :|: ||   ||||| || |||||||||||||| :
Db     69 NISKEEEDIIIKLHATLGNRWSLIASHLPGRTDNEIKNYWNS---------------- 110

Qy    172 KDAMRYLWMPHLADDVDTIA---AANDDDEDHHHNLRLLVLHHHQ----------AQ 215
                  ||:  : |      |  ||    ::  |     :            |
Db    111 ----------HLSRQIHTYRRKYTAGPDDTAIAIDMSKLQSADRRRGGRTPGRPPKASAS 160

Qy    216 HLQQA-AAAAGGAANDLAAGAYDVRQLHAL------PSSGMAATSSSDSLASESYD-DGG 267
            :|| |   || |   || |   |    :      |:|   :| :::    | |  |
Db    161 RTKQADADQPGGEAKGPAAAASSPRHSDVVNPGPNQPNSSSGSTGTAEEEGPSSEDASGP 220

Qy    268 LLFANLRAGEMLMDGGDWAAQQEADQGLWPPPP 300
          :   :  |:::     |        | |  |
Db    221 WVLEPIELGDLV-----WGEADSEMDALMPIGP 248


RESULT   3
GL1_ARATH
ID   GL1_ARATH      STANDARD;      PRT;   228 AA.
AC   P27900;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   TRICHOME DIFFERENTIATION PROTEIN GL1.
GN   GL1.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC   Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92034971; PubMed=1934056;
RA   Oppenheimer D.G., Herman P.L., Sivakumaran S., Esch J., Marks M.D.;
RT   "A myb gene required for leaf trichome differentiation in Arabidopsis
RT   is expressed in stipules.";
RL   Cell 67:483-493(1991).
CC   -!- FUNCTION: REGULATES THE PRODUCTION OF A SIGNAL THAT INDUCES
CC       HAIR (TRICHOME) PRECURSOR CELLS ON LEAF PRIMORDIA TO
CC       DIFFERENTIATE.
CC   -!- SIMILARITY: BELONGS TO THE MYB FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M79448; AAC97387.1; -.
DR   PIR; A39289; TVMUG1.
DR   HSSP; P01103; 1POM.
DR   TRANSFAC; T01588; -.
DR   InterPro; IPR001005; -.
DR   Pfam; PF00249; myb_DNA-binding; 2.
```